Draper

1646

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/920,608*

DATE: 02/11/1999
TIME: 15:29:53

INPUT SET: S30598.raw   P#12

ENTERED

```
 1                            SEQUENCE LISTING
 2
 3   (1)    General Information:
 4
 5       (i) APPLICANT: Pelleymounter, Mary Ann
 6                      Hecht, Randy I
 7                      Mann, Michael B
 8
 9      (ii) TITLE OF INVENTION: OB PROTEIN COMPOSITIONS AND METHODS
10
11     (iii) NUMBER OF SEQUENCES: 6
12
13      (iv) CORRESPONDENCE ADDRESS:
14              (A) ADDRESSEE: Amgen Inc.
15              (B) STREET: 1840 Dehavilland Drive
16              (C) CITY: Thousand Oaks
17              (D) STATE: California
18              (E) COUNTRY: U.S.A.
19              (F) ZIP: 91230-1789
20
21       (v) COMPUTER READABLE FORM:
22              (A) MEDIUM TYPE: Floppy disk
23              (B) COMPUTER: IBM PC compatible
24              (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25              (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
26
27      (vi) CURRENT APPLICATION DATA:
28              (A) APPLICATION NUMBER: US 08/474,833
29              (B) FILING DATE: 07-JUN-1995
30              (C) CLASSIFICATION:
31
32    (viii) ATTORNEY/AGENT INFORMATION:
33              (A) NAME: Pessin, Karol M.
34              (C) REFERENCE/DOCKET NUMBER: A-345
35
36
37   (2) INFORMATION FOR SEQ ID NO:1:
38
39       (i) SEQUENCE CHARACTERISTICS:
40              (A) LENGTH: 491 base pairs
41              (B) TYPE: nucleic acid
42              (C) STRANDEDNESS: double
43              (D) TOPOLOGY: linear
44
45      (ii) MOLECULE TYPE: cDNA
46
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--> (before line 28)

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47
48
49
50        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
51
52    TCTAGATTTG AGTTTTAACT TTTAGAAGGA GGAATAACAT ATGGTACCGA TCCAGAAAGT      60
53
54    TCAGGACGAC ACCAAAACCT TAATTAAAAC GATCGTTACG CGTATCAACG ACATCAGTCA     120
55
56    CACCCAGTCG GTCTCCGCTA AACAGCGTGT TACCGGTCTG GACTTCATCC CGGGTCTGCA     180
57
58    CCCGATCCTA AGCTTGTCCA AAATGGACCA GACCCTGGCT GTATACCAGC AGGTGTTAAC     240
59
60    CTCCCTGCCG TCCCAGAACG TTCTTCAGAT CGCTAACGAC CTCGAGAACC TTCGCGACCT     300
61
62    GCTGCACCTG CTGGCATTCT CCAAATCCTG CTCCCTGCCG CAGACCTCAG GTCTTCAGAA     360
63
64    ACCGGAATCC CTGGACGGGG TCCTGGAAGC ATCCCTGTAC AGCACCGAAG TTGTTGCTCT     420
65
66    GTCCCGTCTG CAGGGTTCCC TTCAGGACAT CCTTCAGCAG CTGGACGTTT CTCCGGAATG     480
67
68    TTAATGGATC C                                                         491
69
70    (2) INFORMATION FOR SEQ ID NO:2:
71
72        (i) SEQUENCE CHARACTERISTICS:
73            (A) LENGTH: 491 base pairs
74            (B) TYPE: nucleic acid
75            (C) STRANDEDNESS: double
76            (D) TOPOLOGY: linear
77
78        (ii) MOLECULE TYPE: cDNA
79
80
81
82
83        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
84
85    AGATCTAAAC TCAAAATTGA AAATCTTCCT CCTTATTGTA TACCATGGCT AGGTCTTTCA      60
86
87    AGTCCTGCTG TGGTTTTGGA ATTAATTTTG CTAGCAATGC GCATAGTTGC TGTAGTCAGT     120
88
89    GTGGGTCAGC CAGAGGCGAT TTGTCGCACA ATGGCCAGAC CTGAAGTAGG GCCCAGACGT     180
90
91    GGGCTAGGAT TCGAACAGGT TTTACCTGGT CTGGGACCGA CATATGGTCG TCCACAATTG     240
92
93    GAGGGACGGC AGGGTCTTGC AAGAAGTCTA GCGATTGCTG GAGCTCTTGG AAGCGCTGGA     300
94
95    CGACGTGGAC GACCGTAAGA GGTTTAGGAC GAGGGACGGC GTCTGGAGTC CAGAAGTCTT     360
96
97    TGGCCTTAGG GACCTGCCCC AGGACCTTCG TAGGGACATG TCGTGGCTTC AACAACGAGA     420
98
99    CAGGGCAGAC GTCCCAAGGG AAGTCCTGTA GGAAGTCGTC GACCTGCAAA GAGGCCTTAC     480
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100
101   AATTACCTAG G                                                          491
102
103   (2)  INFORMATION FOR SEQ ID NO:3:
104
105        (i)  SEQUENCE CHARACTERISTICS:
106             (A)  LENGTH: 147 amino acids
107             (B)  TYPE: amino acid
108             (C)  STRANDEDNESS: single
109             (D)  TOPOLOGY: linear
110
111        (ii)  MOLECULE TYPE: protein
112
113
114
115
116        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:3:
117
118        Met Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys
119        1               5                   10                  15
120
121        Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser
122                20                  25                  30
123
124        Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro
125             35                  40                  45
126
127        Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln
128             50                  55                  60
129
130        Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln Ile Ala Asn Asp
131        65                  70                  75                  80
132
133        Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Phe Ser Lys Ser
134                85                  90                  95
135
136        Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro Glu Ser Leu Asp
137                100                 105                 110
138
139        Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser
140                115                 120                 125
141
142        Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln Leu Asp Val Ser
143                130                 135                 140
144
145        Pro Glu Cys
146        145
147
148   (2)  INFORMATION FOR SEQ ID NO:4:
149
150        (i)  SEQUENCE CHARACTERISTICS:
151             (A)  LENGTH: 454 base pairs
152             (B)  TYPE: nucleic acid
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153               (C) STRANDEDNESS: double
154               (D) TOPOLOGY: linear
155
156        (ii) MOLECULE TYPE: cDNA
157
158
159
160
161        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
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163  CATATGGTAC CGATCCAGAA AGTTCAGGAC GACACCAAAA CCTTAATTAA AACGATCGTT      60
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165  ACGCGTATCA ACGACATCAG TCACACCCAG TCGGTGAGCT CTAAACAGCG TGTTACAGGC     120
166
167  CTGGACTTCA TCCCGGGTCT GCACCCGATC CTGACCTTGT CCAAAATGGA CCAGACCCTG     180
168
169  GCTGTATACC AGCAGATCTT AACCTCCATG CCGTCCCGTA ACGTTCTTCA GATCTCTAAC     240
170
171  GACCTCGAGA ACCTTCGCGA CCTGCTGCAC GTGCTGGCAT TCTCCAAATC CTGCCACCTG     300
172
173  CCATGGGCTT CAGGTCTTGA GACTCTGGAC TCTCTGGGCG GGGTCCTGGA AGCATCCGGT     360
174
175  TACAGCACCG AAGTTGTTGC TCTGTCCCGT CTGCAGGGTT CCCTTCAGGA CATGCTTTGG     420
176
177  CAGCTGGACC TGTCTCCGGG TTGTTAATGG ATCC                                 454
178
179  (2) INFORMATION FOR SEQ ID NO:5:
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181        (i) SEQUENCE CHARACTERISTICS:
182               (A) LENGTH: 454 base pairs
183               (B) TYPE: nucleic acid
184               (C) STRANDEDNESS: double
185               (D) TOPOLOGY: linear
186
187        (ii) MOLECULE TYPE: cDNA
188
189
190
191
192        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
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194  GTATACCATG GCTAGGTCTT TCAAGTCCTG CTGTGGTTTT GGAATTAATT TTGCTAGCAA      60
195
196  TGCGCATAGT TGCTGTAGTC AGTGTGGGTC AGCCACTCGA GATTTGTCGC ACAATGTCCG     120
197
198  GACCTGAAGT AGGGCCCAGA CGTGGGCTAG GACTGGAACA GGTTTTACCT GGTCTGGGAC     180
199
200  CGACATATGG TCGTCTAGAA TTGGAGGTAC GGCAGGGCAT TGCAAGAAGT CTAGAGATTG     240
201
202  CTGGAGCTCT TGGAAGCGCT GGACGACGTG CACGACCGTA AGAGGTTTAG GACGGTGGAC     300
203
204  GGTACCCGAA GTCCAGAACT CTGAGACCTG AGAGACCCGC CCCAGGACCT TCGTAGGCCA     360
205
```

INPUT SET: S30598.raw

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206   ATGTCGTGGC TTCAACAACG AGACAGGGCA GACGTCCCAA GGGAAGTCCT GTACGAAACC      420
207
208   GTCGACCTGG ACAGAGGCCC AACAATTACC TAGG                                    454
209
210   (2) INFORMATION FOR SEQ ID NO:6:
211
212       (i) SEQUENCE CHARACTERISTICS:
213           (A) LENGTH: 147 amino acids
214           (B) TYPE: amino acid
215           (C) STRANDEDNESS: single
216           (D) TOPOLOGY: linear
217
218      (ii) MOLECULE TYPE: protein
219
220
221
222
223      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
224
225       Met Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys
226       1               5                   10                  15
227
228       Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser
229                   20                  25                  30
230
231       Ser Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro
232               35                  40                  45
233
234       Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln
235           50                  55                  60
236
237       Ile Leu Thr Ser Met Pro Ser Arg Asn Val Leu Gln Ile Ser Asn Asp
238       65                  70                  75                  80
239
240       Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys Ser
241                   85                  90                  95
242
243       Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly
244                   100                 105                 110
245
246       Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser
247                   115                 120                 125
248
249       Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu Ser
250                   130                 135                 140
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/08/920,608*

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Line	Error	Original Text
28	Wrong application Serial Number	(A) APPLICATION NUMBER: US 08/474,833